



SEQUENCE LISTING

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WANG, PINGER

<120> TRANSGENIC PLANTS PRODUCING A PAP II PROTEIN

<130> OCIRS 3.9-060 CONT

<140> 09/721,047

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<151> 1998-05-22

<160> 21

<170> PatentIn Ver. 3.3

<210> 1

<211> 1379

<212> DNA

<213> *Phytolacca americana*

<220>

<221> CDS

<222> (225)..(1163)

<400> 1

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atccccgataa acaatacaaaa ttagacaata agatgacata caagtaccta aactgtgtat 120

ggggggagtga aacctcagct gctaaaaaaa cggtgtaaga aaaaaagaaa gttgtgagtt 180

aactacaggg cgaaagtatt ggaactagct agtaggaagg gaag atg aag tcg atg 236
Met Lys Ser Met

1

ctt gtg gtg aca ata tca ata tgg ctc att ctt gca cca act tca act 284
Leu Val Val Thr Ile Ser Ile Trp Leu Ile Leu Ala Pro Thr Ser Thr
5 10 15 20

tgg gct gtg aat aca atc atc tac aat gtt gga agt acc acc att agc 332
Trp Ala Val Asn Thr Ile Ile Tyr Asn Val Gly Ser Thr Thr Ile Ser
25 30 35

aaa tac gcc act ttt ctg aat gat ctt cgt aat gaa gcg aaa gat cca 380
Lys Tyr Ala Thr Phe Leu Asn Asp Leu Arg Asn Glu Ala Lys Asp Pro
40 45 50

agt tta aaa tgc tat gga ata cca atg ctg ccc aat aca aat aca aat 428
Ser Leu Lys Cys Tyr Gly Ile Pro Met Leu Pro Asn Thr Asn Thr Asn
55 60 65

| | |
|---|------|
| cca aag tac gtg ttg gtt gag ctc caa ggt tca aat aaa aaa acc atc | 476 |
| Pro Lys Tyr Val Leu Val Glu Leu Gln Gly Ser Asn Lys Lys Thr Ile | |
| 70 75 80 | |
| aca cta atg ctg aga cga aac aat ttg tat gtg atg ggt tat tct gat | 524 |
| Thr Leu Met Leu Arg Arg Asn Asn Leu Tyr Val Met Gly Tyr Ser Asp | |
| 85 90 95 100 | |
| ccc ttt gaa acc aat aaa tgt cgt tac cat atc ttt aat gat atc tca | 572 |
| Pro Phe Glu Thr Asn Lys Cys Arg Tyr His Ile Phe Asn Asp Ile Ser | |
| 105 110 115 | |
| ggg act gaa cgc caa gat gta gag act act ctt tgc cca aat gcc aat | 620 |
| Gly Thr Glu Arg Gln Asp Val Glu Thr Thr Leu Cys Pro Asn Ala Asn | |
| 120 125 130 | |
| tct cgt gtt agt aaa aac ata aac ttt gat agt cga tat cca aca ttg | 668 |
| Ser Arg Val Ser Lys Asn Ile Asn Phe Asp Ser Arg Tyr Pro Thr Leu | |
| 135 140 145 | |
| gaa tca aaa gcg gga gta aaa tca aga agt cag gtc caa ctg gga att | 716 |
| Glu Ser Lys Ala Gly Val Lys Ser Arg Ser Gln Val Gln Leu Gly Ile | |
| 150 155 160 | |
| caa ata ctc gac agt aat att gga aag att tct gga gtg atg tca ttc | 764 |
| Gln Ile Leu Asp Ser Asn Ile Gly Lys Ile Ser Gly Val Met Ser Phe | |
| 165 170 175 180 | |
| act gag aaa acc gaa gcc gaa ttc cta ttg gta gcc ata caa atg gta | 812 |
| Thr Glu Lys Thr Glu Ala Glu Phe Leu Leu Val Ala Ile Gln Met Val | |
| 185 190 195 | |
| tca gag gca gca aga ttc aag tac ata gag aat cag gtg aaa act aat | 860 |
| Ser Glu Ala Ala Arg Phe Lys Tyr Ile Glu Asn Gln Val Lys Thr Asn | |
| 200 205 210 | |
| ttt aac aga gca ttc aac cct aat ccc aaa gta ctt aat ttg caa gag | 908 |
| Phe Asn Arg Ala Phe Asn Pro Asn Pro Lys Val Leu Asn Leu Gln Glu | |
| 215 220 225 | |
| aca tgg ggt aag att tca aca gca att cat gat gcc aag aat gga gtt | 956 |
| Thr Trp Gly Lys Ile Ser Thr Ala Ile His Asp Ala Lys Asn Gly Val | |
| 230 235 240 | |
| tta ccc aaa cct ctc gag cta gtg gat gcc agt ggt gcc aag tgg ata | 1004 |
| Leu Pro Lys Pro Leu Glu Leu Val Asp Ala Ser Gly Ala Lys Trp Ile | |
| 245 250 255 260 | |
| gtg ttg aga gtg gat gaa atc aag cct gat gta gca ctc tta aac tac | 1052 |
| Val Leu Arg Val Asp Glu Ile Lys Pro Asp Val Ala Leu Leu Asn Tyr | |
| 265 270 275 | |
| gtt ggt ggg agc tgt cag aca act tat aac caa aat gcc atg ttt cct | 1100 |
| Val Gly Gly Ser Cys Gln Thr Thr Tyr Asn Gln Asn Ala Met Phe Pro | |
| 280 285 290 | |

caa ctt ata atg tct act tat tat aat tac atg gtt aat ctt ggt gat 1148
 Gln Leu Ile Met Ser Thr Tyr Tyr Asn Tyr Met Val Asn Leu Gly Asp
 295 300 305

cta ttt gaa gga ttc tgatcataaa cataataagg agtatatata tattactcca 1203
 Leu Phe Glu Gly Phe
 310

actatattat aaagcttaaa taagaggccg tgtaattag tacttggtgc cttttgcttt 1263

atggtgttgt ttattatgcc ttgtatgctt gtaatattat ctagagaaca agatgtactg 1323

tgtaatagtc ttgtttgaaa taaaacttcc aattatgatg caaaaaaaaa aaaaaa 1379

<210> 2

<211> 313

<212> PRT

<213> *Phytolacca americana*

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Pro Thr Ser Thr Trp Ala Val Asn Thr Ile Ile Tyr Asn Val Gly Ser
 20 25 30

Thr Thr Ile Ser Lys Tyr Ala Thr Phe Leu Asn Asp Leu Arg Asn Glu
 35 40 45

Ala Lys Asp Pro Ser Leu Lys Cys Tyr Gly Ile Pro Met Leu Pro Asn
 50 55 60

Thr Asn Thr Asn Pro Lys Tyr Val Leu Val Glu Leu Gln Gly Ser Asn
 65 70 75 80

Lys Lys Thr Ile Thr Leu Met Leu Arg Arg Asn Asn Leu Tyr Val Met
 85 90 95

Gly Tyr Ser Asp Pro Phe Glu Thr Asn Lys Cys Arg Tyr His Ile Phe
 100 105 110

Asn Asp Ile Ser Gly Thr Glu Arg Gln Asp Val Glu Thr Thr Leu Cys
 115 120 125

Pro Asn Ala Asn Ser Arg Val Ser Lys Asn Ile Asn Phe Asp Ser Arg
 130 135 140

Tyr Pro Thr Leu Glu Ser Lys Ala Gly Val Lys Ser Arg Ser Gln Val
 145 150 155 160

Gln Leu Gly Ile Gln Ile Leu Asp Ser Asn Ile Gly Lys Ile Ser Gly
 165 170 175

Val Met Ser Phe Thr Glu Lys Thr Glu Ala Glu Phe Leu Leu Val Ala
 180 185 190

Ile Gln Met Val Ser Glu Ala Ala Arg Phe Lys Tyr Ile Glu Asn Gln
 195 200 205

Val Lys Thr Asn Phe Asn Arg Ala Phe Asn Pro Asn Pro Lys Val Leu
 210 215 220

Asn Leu Gln Glu Thr Trp Gly Lys Ile Ser Thr Ala Ile His Asp Ala
 225 230 235 240

Lys Asn Gly Val Leu Pro Lys Pro Leu Glu Leu Val Asp Ala Ser Gly
 245 250 255

Ala Lys Trp Ile Val Leu Arg Val Asp Glu Ile Lys Pro Asp Val Ala
 260 265 270

Leu Leu Asn Tyr Val Gly Gly Ser Cys Gln Thr Thr Tyr Asn Gln Asn
 275 280 285

Ala Met Phe Pro Gln Leu Ile Met Ser Thr Tyr Tyr Asn Tyr Met Val
 290 295 300

Asn Leu Gly Asp Leu Phe Glu Gly Phe
 305 310

<210> 3
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 <213> *Phytolacca americana*

<220>
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 <222> (1)..(930)

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 Met Lys Met Lys Val Leu Glu Val Val Gly Leu Ala Ile Ser Ile Trp
 -25 -20 -15 -10

ctg atg ctt aca cca cca gct tct tca aac ata gtg ttt gac gtt gag 96
 Leu Met Leu Thr Pro Pro Ala Ser Ser Asn Ile Val Phe Asp Val Glu
 -5 -1 1 5

aat gcc aca cca gaa acc tac tct aat ttt ctg act agt ttg cga gaa 144
 Asn Ala Thr Pro Glu Thr Tyr Ser Asn Phe Leu Thr Ser Leu Arg Glu
 10 15 20

gct gtg aaa gac aag aaa ttg aca tgc cat gga atg ata atg gcc aca 192
 Ala Val Lys Asp Lys Lys Leu Thr Cys His Gly Met Ile Met Ala Thr
 25 30 35

| | |
|---|-----|
| acc ctc act gaa caa ccc aag tat gtg ttg gtt gac ctc aaa ttc gga | 240 |
| Thr Leu Thr Glu Gln Pro Lys Tyr Val Leu Val Asp Leu Lys Phe Gly | |
| 40 45 50 55 | |
| tct gga aca ttc aca tta gca atc aga agg gga aac tta tat ttg gag | 288 |
| Ser Gly Thr Phe Thr Leu Ala Ile Arg Arg Gly Asn Leu Tyr Leu Glu | |
| 60 65 70 | |
| ggc tat tct gac att tac aat gga aaa tgt cgt tat cgg atc ttc aag | 336 |
| Gly Tyr Ser Asp Ile Tyr Asn Gly Lys Cys Arg Tyr Arg Ile Phe Lys | |
| 75 80 85 | |
| gat tca gaa tcc gat gcc caa gag acc gtt tgc ccc ggg gac aaa agc | 384 |
| Asp Ser Glu Ser Asp Ala Gln Glu Thr Val Cys Pro Gly Asp Lys Ser | |
| 90 95 100 | |
| aag cct ggc act cag aat aat atc ccc tat gaa aag agt tac aaa ggg | 432 |
| Lys Pro Gly Thr Gln Asn Asn Ile Pro Tyr Glu Lys Ser Tyr Lys Gly | |
| 105 110 115 | |
| atg gaa tca aag ggt ggg gct aga act aaa tta ggg tta gga aag ata | 480 |
| Met Glu Ser Lys Gly Gly Ala Arg Thr Lys Leu Gly Leu Gly Lys Ile | |
| 120 125 130 135 | |
| aca ctc aag agt cga atg ggt aaa atc tac ggc aag gat gca acg gat | 528 |
| Thr Leu Lys Ser Arg Met Gly Lys Ile Tyr Gly Lys Asp Ala Thr Asp | |
| 140 145 150 | |
| cag aag cag tat caa aaa aat gag gct gaa ttt ctt ctt ata gcc gtt | 576 |
| Gln Lys Gln Tyr Gln Lys Asn Glu Ala Glu Phe Leu Leu Ile Ala Val | |
| 155 160 165 | |
| caa atg gtt act gag gca tca agg ttc aaa tac att gag aac aaa gtg | 624 |
| Gln Met Val Thr Glu Ala Ser Arg Phe Lys Tyr Ile Glu Asn Lys Val | |
| 170 175 180 | |
| aag gct aaa ttt gat gat gcc aat ggg tat cag cca gat cct aaa gct | 672 |
| Lys Ala Lys Phe Asp Asp Ala Asn Gly Tyr Gln Pro Asp Pro Lys Ala | |
| 185 190 195 | |
| att tcc cta gag aaa aat tgg gac agt gtt tct aag gtc att gca aaa | 720 |
| Ile Ser Leu Glu Lys Asn Trp Asp Ser Val Ser Lys Val Ile Ala Lys | |
| 200 205 210 215 | |
| gtt ggc acc tcc ggt gat agt act gtt act tta cct gga gac cta aaa | 768 |
| Val Gly Thr Ser Gly Asp Ser Thr Val Thr Leu Pro Gly Asp Leu Lys | |
| 220 225 230 | |
| gat gag aat aat aaa cct tgg act acg gcc acc atg aac gac ctt aag | 816 |
| Asp Glu Asn Asn Lys Pro Trp Thr Thr Ala Thr Met Asn Asp Leu Lys | |
| 235 240 245 | |
| aac gac att atg gca ctc cta acc cac gtt act tgc aag gtt aaa agt | 864 |
| Asn Asp Ile Met Ala Leu Leu Thr His Val Thr Cys Lys Val Lys Ser | |
| 250 255 260 | |

tcc atg ttc cct gaa att atg tcc tat tat tat agg act agt att agt 912
 Ser Met Phe Pro Glu Ile Met Ser Tyr Tyr Tyr Arg Thr Ser Ile Ser
 265 270 275

aac ctt ggt gaa ttc gag tgat 934
 Asn Leu Gly Glu Phe Glu
 280 285

<210> 4
 <211> 310
 <212> PRT
 <213> *Phytolacca americana*

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 -5 -1 1 5
 Asn Ala Thr Pro Glu Thr Tyr Ser Asn Phe Leu Thr Ser Leu Arg Glu
 10 15 20
 Ala Val Lys Asp Lys Lys Leu Thr Cys His Gly Met Ile Met Ala Thr
 25 30 35
 Thr Leu Thr Glu Gln Pro Lys Tyr Val Leu Val Asp Leu Lys Phe Gly
 40 45 50 55
 Ser Gly Thr Phe Thr Leu Ala Ile Arg Arg Gly Asn Leu Tyr Leu Glu
 60 65 70
 Gly Tyr Ser Asp Ile Tyr Asn Gly Lys Cys Arg Tyr Arg Ile Phe Lys
 75 80 85
 Asp Ser Glu Ser Asp Ala Gln Glu Thr Val Cys Pro Gly Asp Lys Ser
 90 95 100
 Lys Pro Gly Thr Gln Asn Asn Ile Pro Tyr Glu Lys Ser Tyr Lys Gly
 105 110 115
 Met Glu Ser Lys Gly Gly Ala Arg Thr Lys Leu Gly Leu Gly Lys Ile
 120 125 130 135
 Thr Leu Lys Ser Arg Met Gly Lys Ile Tyr Gly Lys Asp Ala Thr Asp
 140 145 150
 Gln Lys Gln Tyr Gln Lys Asn Glu Ala Glu Phe Leu Leu Ile Ala Val
 155 160 165
 Gln Met Val Thr Glu Ala Ser Arg Phe Lys Tyr Ile Glu Asn Lys Val
 170 175 180
 Lys Ala Lys Phe Asp Asp Ala Asn Gly Tyr Gln Pro Asp Pro Lys Ala
 185 190 195

Ile Ser Leu Glu Lys Asn Trp Asp Ser Val Ser Lys Val Ile Ala Lys
 200 205 210 215
 Val Gly Thr Ser Gly Asp Ser Thr Val Thr Leu Pro Gly Asp Leu Lys
 220 225 230
 Asp Glu Asn Asn Lys Pro Trp Thr Thr Ala Thr Met Asn Asp Leu Lys
 235 240 245
 Asn Asp Ile Met Ala Leu Leu Thr His Val Thr Cys Lys Val Lys Ser
 250 255 260
 Ser Met Phe Pro Glu Ile Met Ser Tyr Tyr Tyr Arg Thr Ser Ile Ser
 265 270 275
 Asn Leu Gly Glu Phe Glu
 280 285

<210> 5
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 Oligonucleotide

<400> 5
 gggttggttca gtgagggttg tggcc 25

<210> 6
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 6
 tttggaggac tattctgac 19

<210> 7
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 7
 gtcagaatag tcctccaaa 19

<210> 8
 <211> 32
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 8
 ccgttcaaat gggtactgtg gcatcaaggt tc 32

<210> 9
 <211> 32
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 9
 gaaccttgat gccacagtaa ccatttgaac gg 32

<210> 10
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 10
 aaaccttaga ctacggccac 20

<210> 11
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 11
 gtggccgtag tctaaggttt 20

<210> 12
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 12
 aaaccttaga ctacggccac 20

<210> 13
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 13
 gtggccgtag tcctagggtt 20

<210> 14
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 14
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<210> 15
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

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<210> 16
 <211> 34
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 16
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<210> 17
 <211> 34
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 17
gcaagtaacg tgggttcgga gtgccataat gtcg 34

<210> 18
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 18
cacgttactt gctaggttaa aagttccatg ttcc 34

<210> 19
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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 19
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<210> 20
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<213> *Phytolacca americana*

<220>
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<222> (1)..(855)

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ttt ctg act agt ttg cga gaa gct gtg aaa gac aag aaa ttg aca tgc 96
Phe Leu Thr Ser Leu Arg Glu Ala Val Lys Asp Lys Lys Leu Thr Cys
20 25 30
cat gga atg ata atg gcc aca acc ctc act gaa caa ccc aag tat gtg 144
His Gly Met Ile Met Ala Thr Thr Leu Thr Glu Gln Pro Lys Tyr Val
35 40 45
ttg gtt gac ctc aaa ttc gga tct gga aca ttc aca tta gca atc aga 192
Leu Val Asp Leu Lys Phe Gly Ser Gly Thr Phe Thr Leu Ala Ile Arg
50 55 60
agg gga aac tta tat ttg gag ggc tat tct gac att tac aat gga aaa 240
Arg Gly Asn Leu Tyr Leu Glu Gly Tyr Ser Asp Ile Tyr Asn Gly Lys
65 70 75 80

| | |
|---|-----|
| tgt cgt tat cgg atc ttc aag gat tca gaa tcc gat gcc caa gag acc | 288 |
| Cys Arg Tyr Arg Ile Phe Lys Asp Ser Glu Ser Asp Ala Gln Glu Thr | |
| 85 90 95 | |
| gtt tgc ccc ggg gac aaa agc aag cct ggc act cag aat aat atc ccc | 336 |
| Val Cys Pro Gly Asp Lys Ser Lys Pro Gly Thr Gln Asn Asn Ile Pro | |
| 100 105 110 | |
| tat gaa aag agt tac aaa ggg atg gaa tca aag ggt ggg gct aga act | 384 |
| Tyr Glu Lys Ser Tyr Lys Gly Met Glu Ser Lys Gly Gly Ala Arg Thr | |
| 115 120 125 | |
| aaa tta ggg tta gga aag ata aca ctc aag agt cga atg ggt aaa atc | 432 |
| Lys Leu Gly Leu Gly Lys Ile Thr Leu Lys Ser Arg Met Gly Lys Ile | |
| 130 135 140 | |
| tac ggc aag gat gca acg gat cag aag cag tat caa aaa aat gag gct | 480 |
| Tyr Gly Lys Asp Ala Thr Asp Gln Lys Gln Tyr Gln Lys Asn Glu Ala | |
| 145 150 155 160 | |
| gaa ttt ctt ctt ata gcc gtt caa atg gtt act gag gca tca agg ttc | 528 |
| Glu Phe Leu Leu Ile Ala Val Gln Met Val Thr Glu Ala Ser Arg Phe | |
| 165 170 175 | |
| aaa tac att gag aac aaa gtg aag gct aaa ttt gat gat gcc aat ggg | 576 |
| Lys Tyr Ile Glu Asn Lys Val Lys Ala Lys Phe Asp Asp Ala Asn Gly | |
| 180 185 190 | |
| tat cag cca gat cct aaa gct att tcc cta gag aaa aat tgg gac agt | 624 |
| Tyr Gln Pro Asp Pro Lys Ala Ile Ser Leu Glu Lys Asn Trp Asp Ser | |
| 195 200 205 | |
| gtt tct aag gtc att gca aaa gtt ggc acc tcc ggt gat agt act gtt | 672 |
| Val Ser Lys Val Ile Ala Lys Val Gly Thr Ser Gly Asp Ser Thr Val | |
| 210 215 220 | |
| act tta cct gga gac cta aaa gat gag aat aat aaa cct tgg act acg | 720 |
| Thr Leu Pro Gly Asp Leu Lys Asp Glu Asn Asn Lys Pro Trp Thr Thr | |
| 225 230 235 240 | |
| gcc acc atg aac gac ctt aag aac gac att atg gca ctc cta acc cac | 768 |
| Ala Thr Met Asn Asp Leu Lys Asn Asp Ile Met Ala Leu Leu Thr His | |
| 245 250 255 | |
| gtt act tgc aag gtt aaa agt tcc atg ttc cct gaa att atg tcc tat | 816 |
| Val Thr Cys Lys Val Lys Ser Ser Met Phe Pro Glu Ile Met Ser Tyr | |
| 260 265 270 | |
| tat tat agg act agt att agt aac ctt ggt gaa ttc gag | 855 |
| Tyr Tyr Arg Thr Ser Ile Ser Asn Leu Gly Glu Phe Glu | |
| 275 280 285 | |

<210> 21

<211> 285

<212> PRT

<213> *Phytolacca americana*

<400> 21

| | | | | | | | | | | | | | | | |
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| Asn | Ile | Val | Phe | Asp | Val | Glu | Asn | Ala | Thr | Pro | Glu | Thr | Tyr | Ser | Asn |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Phe | Leu | Thr | Ser | Leu | Arg | Glu | Ala | Val | Lys | Asp | Lys | Lys | Leu | Thr | Cys |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| His | Gly | Met | Ile | Met | Ala | Thr | Thr | Leu | Thr | Glu | Gln | Pro | Lys | Tyr | Val |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Leu | Val | Asp | Leu | Lys | Phe | Gly | Ser | Gly | Thr | Phe | Thr | Leu | Ala | Ile | Arg |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Arg | Gly | Asn | Leu | Tyr | Leu | Glu | Gly | Tyr | Ser | Asp | Ile | Tyr | Asn | Gly | Lys |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 |
| Cys | Arg | Tyr | Arg | Ile | Phe | Lys | Asp | Ser | Glu | Ser | Asp | Ala | Gln | Glu | Thr |
| | | | | 85 | | | | | 90 | | | | | 95 | |
| Val | Cys | Pro | Gly | Asp | Lys | Ser | Lys | Pro | Gly | Thr | Gln | Asn | Asn | Ile | Pro |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Tyr | Glu | Lys | Ser | Tyr | Lys | Gly | Met | Glu | Ser | Lys | Gly | Gly | Ala | Arg | Thr |
| | | 115 | | | | | 120 | | | | | 125 | | | |
| Lys | Leu | Gly | Leu | Gly | Lys | Ile | Thr | Leu | Lys | Ser | Arg | Met | Gly | Lys | Ile |
| | 130 | | | | | 135 | | | | | 140 | | | | |
| Tyr | Gly | Lys | Asp | Ala | Thr | Asp | Gln | Lys | Gln | Tyr | Gln | Lys | Asn | Glu | Ala |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 |
| Glu | Phe | Leu | Leu | Ile | Ala | Val | Gln | Met | Val | Thr | Glu | Ala | Ser | Arg | Phe |
| | | | | 165 | | | | | 170 | | | | | 175 | |
| Lys | Tyr | Ile | Glu | Asn | Lys | Val | Lys | Ala | Lys | Phe | Asp | Asp | Ala | Asn | Gly |
| | | | 180 | | | | | 185 | | | | | 190 | | |
| Tyr | Gln | Pro | Asp | Pro | Lys | Ala | Ile | Ser | Leu | Glu | Lys | Asn | Trp | Asp | Ser |
| | | 195 | | | | | 200 | | | | | 205 | | | |
| Val | Ser | Lys | Val | Ile | Ala | Lys | Val | Gly | Thr | Ser | Gly | Asp | Ser | Thr | Val |
| | 210 | | | | | 215 | | | | | 220 | | | | |
| Thr | Leu | Pro | Gly | Asp | Leu | Lys | Asp | Glu | Asn | Asn | Lys | Pro | Trp | Thr | Thr |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 |
| Ala | Thr | Met | Asn | Asp | Leu | Lys | Asn | Asp | Ile | Met | Ala | Leu | Leu | Thr | His |
| | | | | 245 | | | | | 250 | | | | | 255 | |
| Val | Thr | Cys | Lys | Val | Lys | Ser | Ser | Met | Phe | Pro | Glu | Ile | Met | Ser | Tyr |
| | | | 260 | | | | | 265 | | | | | 270 | | |
| Tyr | Tyr | Arg | Thr | Ser | Ile | Ser | Asn | Leu | Gly | Glu | Phe | Glu | | | |
| | | 275 | | | | | 280 | | | | | 285 | | | |